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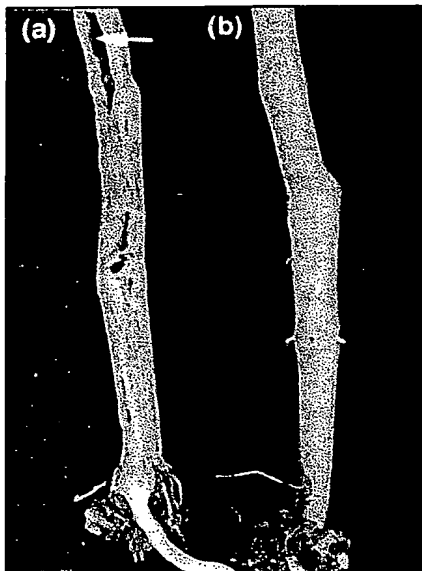
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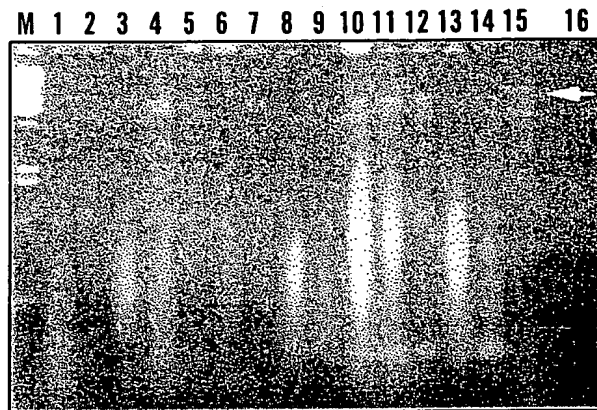
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1/16

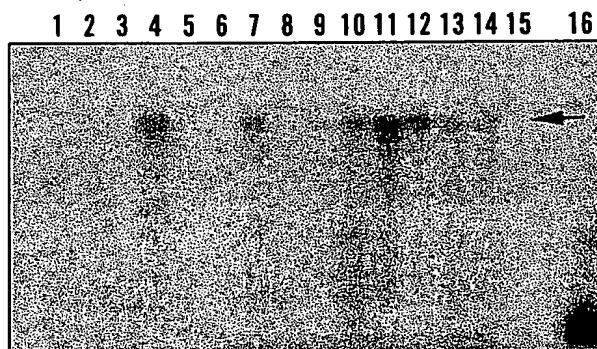


***FIG. 1***

2/16

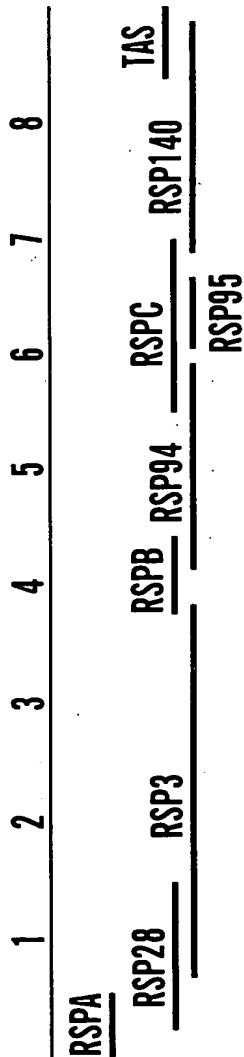


**FIG. 2A**

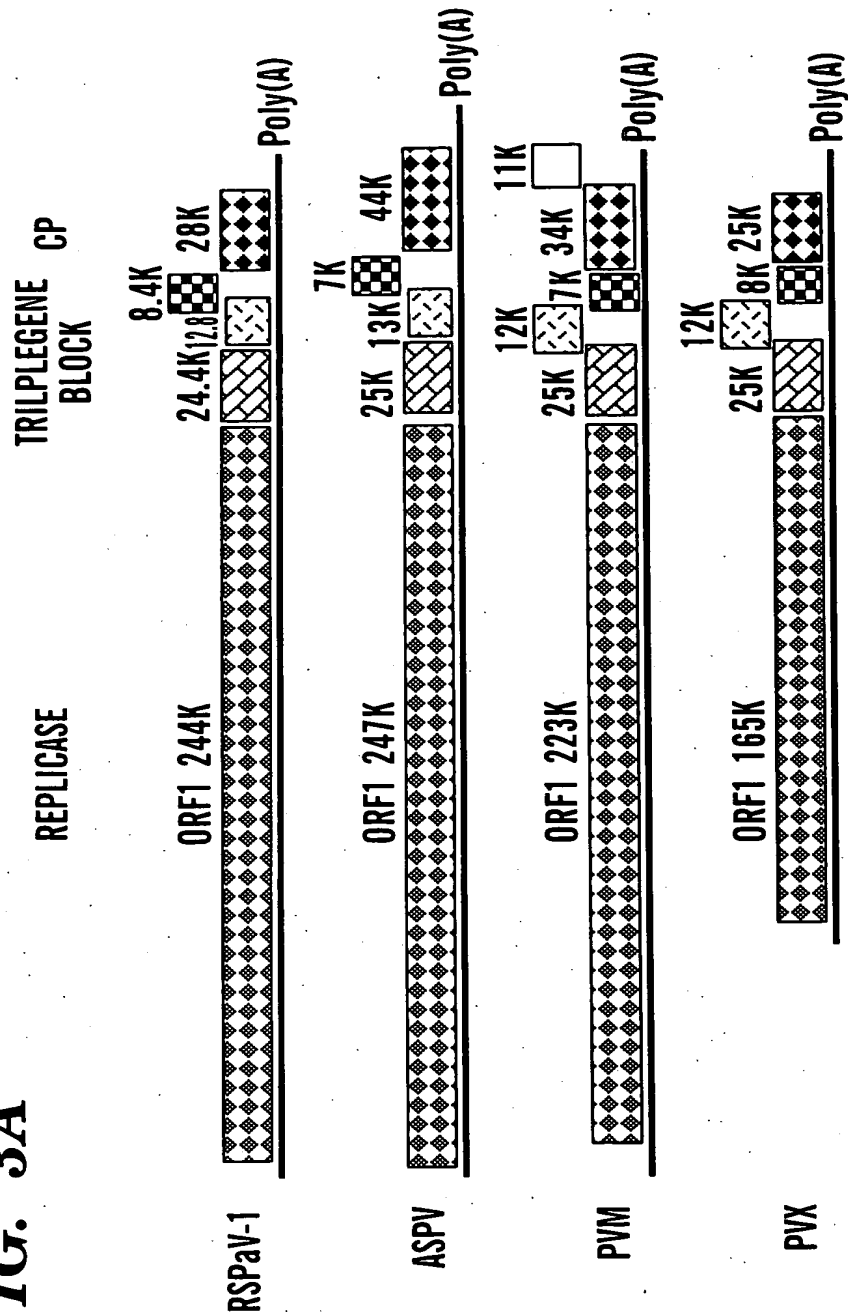


**FIG. 2B**

3/16



**FIG. 3A**



**FIG. 3B**

4/16

FIG. 4A

MA\*.#R.\*E\*\*.\*F\*\*.\*Q\*\*.\*A\*\*.\*E#\*\*.\*F\*\*.\*L\*\*.\*K.\*L\*\*.\*GIYLS#S\*\*.  
(1)MAVTYRTPMEDI VNCFE- PATQAVI ANSAATLYKNFEENHCQFNY- LSPLAKRKLSMAGI YLSPYS AVV  
(1)MALLSRTAAEEVI ASFT- SEEQSRI STQAVLALTNVEKDKHDLFNALPELAKMRLFNSGI YLSPHSYRP  
(1)MALSYPRAVEEVLAFT- SDEQSRVSATALKALVDLEESQHNLFSAFPDRSKERLI SSGI YLSPYSFRP

Consensus  
PVM Rep-1  
ASP Rep-1  
RSPaV-1 Rep-1

HSHPVCKTLEN. IL#N#LPSY. -#\*SFY#V#IK. K##\*LK\*\*.\*#L\*\*.\*V\*\*.\*NR\*\*.\*S.D..RY\*..F#  
HSHPVCKTLENYI LYSVLPSYI- NSSFYFVGI KERKQLLKSCKNLDVQVNNRYVTS ADRMRYTNDFF  
HSHPVCKTLENNI LFNILPSYL- DNSFYLVSI KKNKVDFLKRHPDLQMVETI NRYI SSI DKTRYGGFFH  
HSHPVCKTLENHILYNVLP SYV- NNSFYFVGI KDFKLQLKRRNKDLSLVALI NRFVTSRDVSRYGSEFV

Consensus  
PVM Rep-1  
ASP Rep-1  
RSPaV-1 Rep-1

\*.S...\*...\*#G.#-D...L#.L#\*...\*#F.HDE.HYW#...LI.-FLD#.\*P...#L\*#  
PYGS...YEHECLVHKGVGLDNEALRGLVGPLRRHKAKNLFHDELHYWSSKVLID-FLDVMRPDKLLGT  
VSPSKI SAKFKCDRTGFE- DDASLI DLI PGCMEGARKRFFHDELHYWTKALIT-FLDHVKPEVMLAS  
ISSDDKSSQVVS..RKGI G-DSNTLRLVPRVI STGARNLFLHDEI HYWSISDLIN-FLDVAKPSMLLAT

Consensus  
PVM Rep-1  
ASP Rep-1  
RSPaV-1 Rep-1

V.PPE.L.G..ESLNPW.Y.Y.I.G..L.F.PDG...E.Y.QPL...YLL.ARS..LPDG...Y.VD...  
VVYPPELLFKPTRSLNEWCYTYDI VGDTLMFFPDGVQSEGYQQLKGGYLLGARSCLKLPDGTVYMDVLC  
IVFPPEI LAGAKESLNPWCYTFR I VGKDLVFFPDGEQSEAYI QPVAGSYLLRTGKI TTPSGDI FQLDLLK  
AVIPPEVLVGPSPESLNPWAYQYKINGNQLLFAPDGNWNEMYSQPLSCRYLLKARSVVLDPGSRYSVDIIH

Consensus  
PVM Rep-1  
ASP Rep-1  
RSPaV-1 Rep-1

S#F\*HHL.S.T..G.....\*R.F.\*F.A...\*L.\*L#\*...\*#P#...\*#KI.Y.YLRTLKKPD..  
SKFPHHLISIT-KGEAAPTHRAFPGFEAVASEALKATLSPDYPCAFPVSYEVENKI YRYLRTLKKPDEQ  
SSFSSHHLISIT-KGEAI GQKMRFFNGFEAVAMKGLNP.LRRKVESCLPI SKNTI LKI YRYLRTLKKPDLQ  
SKFSSHLLSFTPMGNLLTSNMRCFSGFDAI GIKDLEP.LSRGMHSCFPVHHDVVTKI YLYLRTLKKPDKE

Consensus  
PVM Rep-1  
ASP Rep-1  
RSPaV-1 Rep-1

SA.AKL.Q.#...P.G#EI\*F.E.F\*.L##✓  
SAIAKLSQII AEPSGREI DFVECFARLVI (371)✓  
SAMAKLSQVCKDPNGYEI KFFEFSKLCL (373)✓  
SAEAKLRQLIEKPTGREIKFIEDFSSSLVI (372)✓

Consensus  
PVM Rep-1  
ASP Rep-1  
RSPaV-1 Rep-1

\*GTFG.GKS.L.-K.\*.#.\*.GK.\*FVSPRR#LA.\*\*#.\*\*\*#K#G.\*\*...V.T\*E.  
 ((1163)I VGTFGSGKSTLF-KNLLKYGAGKSLDFVSPRRALAEF KRTVGMNERGGRAKAGQE...NWRVTTLET  
 ((1372)I LGTFGCGKSSLF-KKFI EKSPGKAITFVSPRRSLAESI NHDGLGLARVGGK-KTGKS KDLKNVRVKT FEL  
 ((1354)V LGTFGAGKSF LY-KSFMKRSEGKFVTFVSPRRALANSI KNDLEMDDSCKVAKAGRSKKEGWD-VVTFEV

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-I Rep-II

F#...#...G#.V#.DE.QL\*PPGY\*DL...\*...#...\*...GDP\*QS.YD#.DR.###...\*...\*...  
 FLARVEFLTEGQVVLDEMQLYPPGYFDLVVSMKVDVRLFLVGDPAQSDYDSEKDRLLVGAMEENMSVV  
 FFLHLDSIKEGHTVVIDEIQLFPPGYIDLII LGLKPNVNI I AGDPCQSDYDCSSDRHI FAGSES DI MRI  
 FLRKVAGLKAGHCVI FDEVQLFPPGYI DLCLLI I RSDAFI SLAGDPCQSTYDSQKDRAILGAEQSDI LRL

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-1 Rep-II

[illegible]

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-1 Rep-II

\*V...\*...#T#GESTGL\*F..G.I\*#.#...S...T.\*RRW.TAL\*RF\*#.#...#N..G.....\*\*  
VVCAHLPEA- KVLTFGESTGLTFMHGTI YISAVSERTNERRW TALRRFRFNLCFVNCSGMDYQQLAGRY  
I VAAHLGLKMKCI TYGESTGLNFQKGAI LVTYESALTS DRRWWTALSRFSHDI.HFI NGMGVTWDNAI THF  
I VQSYFGMKQLTLTFGESTGLNFKNGGI LISHDSFHTDDRRWLTALSRFSHNLDL VNI TGLRVESFLSHF

Consensus  
PVM Rep-II  
ASPv Rep-II  
RSPaV-1 Rep-II

G\*\*\*F#.....\*\*LPG.\*#.#...#G#.EGVRE#KL.GDPWLK.M.\*L\*Q...\*.E..\*#.  
KGRVRSKFLCKTAIPDDLNSMLPGQALFKSEYPRLI GKDEGVREEKLAGDPWLKTM NLYQAPEVEIAEE  
VVGKPLHKFFTKRACNDIIDLPGRPELIEGFSQVGADGVREAKLVGDPWLKTKI FLGQNPDFEIEIA  
AGKPLYHFLTAKSGENVIDLLPGEPNFFSGFNVSIGKNEGVREEKCGDPWLKVML FLGQDEDCVEEEM

Consensus  
PVM Rep-II  
ASPv Rep-II  
RSPaV-I Rep-II

E#WF\*TH\*P...LE#.RA.WV.K...#E#RE#R.G...\*.QF.\*H....G...#.L.NA.ER#E.  
PEVVMQEEWFRTHLPRDELESVRAQVWHKILAKEYREVVRMGDMVSEQFTHDHTKQLGAKQLTNAAEFET  
DEVEAAEDWFKTHIPIMSLEAVRAQVWHKILSREDREFRIGDI TTEQFTDDHSKNRGQ.ELTNAAEVYEA  
E#E#ECSNEEWFKTHIPLSNLESTRARVWGKMLKEYREVRCGYEMTQQFFDEHRTGTGE-QLSNACERFES

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-1 Rep-II

6/16

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-I Rep-II  
IYPRH\*..D..TFLMAV.KRL.FS.P..E..\*\*L\*\*A\*\*GK\*LL\*.FL...PL#. \*H#...\*...EA\*...F  
IYPRHRASDTVTFLMAVKKRLSFSNPGEKGNLFHAASYGKALLSEFLKRVPLKPNHNVRFMEEAL-WNF  
IYPRHKGTDATFLMAVKKRLSFSPPAAEHAKLRRAKPFGKFLDFTFLKRVPLNSSSHDEKMMQEA-V-HAF  
IYPRHKGNDISI TFLMAVRKRLKFSKPQVEAAKLRRAKPYGKFLDSDSFLSKIPLKASHNSI MFHEAV-QEF

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-I Rep-II  
E.KK.SKS#ATIENH.GRSC#DW..D#A\*IF\*KSQ.CTKFDNR..R#AKA\*Q\*\*\*CFQH#VL.RFAPYMR  
EEKKLSKSAATIENHSGRSCRDWPTDVAQIFSKSQLCTKFDNR-FRVAKAAQSI VCFQHAVLCRFAPYMR  
EEKKLSKSMATIENHSGRSCEDWPVDKALIFMKSQCTKFDNR-FRSKAGQTLACFQHSVLCRFAPYMR  
EAKKASKSAATIENHAGRSCRDWLLDVALIFMKSQHCTKFDNR-LRVAKAGQTLACFQHAVLVRFAPYMR

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-I Rep-II  
YIE.K....L..N.YIHSGK##\*#L..WV.\*...F.\*#CTESDYEAFDASQD\*FI\*AFEL..MK\*L\*LP.  
YIEMKVHEVLPKNYYIHSGKGLEELDAAWKKGK-FDRICTESDYEAFDASQDEFIMAFELELMKYLRPLPS  
YIESKVTEVLPKNLYIHSGKNIDDLAAWVTTSK-FNGVCTESDYEAFDASQDHFI LAFELEVMMKFLGLPS  
YIEKKLMQALKPNFYIHSGKGLDELNEWVTRG-FTGICTESDYEAFDASQDHFI LAFELQIMKFLGLPE

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-I Rep-II  
DLI.DY.FIK.\*LGSKLG\*F.I.MRF\*GEASTFLFNT\*ANMLFTF\*RY.\*.G.E.I.FAGDDMCA\*#RL..  
DLIEDYKFIKTSLSGKLGNFAMRFSGEASTFLFNTLANMLFTFMRYNIRGDEFICFAGDDMCASRRLLQ  
DLIADYTFIKTHLSGKLGSAIMRFTGEASTFLFNTMANMLFTFLRYDLNGREAI CFAGDDMCANSRLKV  
DLILDYEFIKIHLGSKLGFSIMRFTGEASTFLFNTMANMLFTFLRYELTGSESI AFAGDDMCANRRRL

B

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-I Rep-II  
.....FL..I.LKAKVQF#.....PTFCGW.L...G#\*KKP#L...ER.#IA\*E#.NL\*NCIDNYAIE  
TKKFAHFLDKLKLKAKVQFVQFVN..KPTFCGWHLCPDGIYKKPQLVLERMCI AKEMNLSNCIDNYAIE  
TNRFSNFLDKIKLAKVQFTAT.....PTFCGWGLCEHGVFKKPPDLVLERLQI ARETRNLENCIDNYAIE  
KTEHEGFLNMI CLKAKVQFVSN.....PTFCGWCLFKEGIFKKPQLI WERICI AREMGNLENCIDNYAIE

Consensus  
PVM Rep-II  
ASPV Rep-II  
RSPaV-I Rep-II  
V\*#AY.#GE.#...#\*##EV.A\*YNCVR\*.V\*##H  
VAYAYKLGEKAVNRMDEEEVAAFYNCVRIIVRNKH  
VSCAYKMGENLNL YLTPQEVDAHYNVCVRFIVQHNH  
VSYAYRLGELAIEMMTEEEVEAHYNVCVRFIVRNKH

FIG. 4C

7/16

Consensus M...#...L...\*F...L...P.V.H.VPG\*GK##LI##...#...A.T#GV\*#.#.#.G.\*I\*...  
PVM25K MDVI VDLLYKYKFERLSNKL.VCPI VVHCVP GAGKSSLI RELLEDSRF CAYTAGVEDQPRLSGNWI RKW  
ASPV25K METVLSLLNEFGFERTVEPL.SDPI VVHAVPGSGKTTLI KQALI RNNI EAVTFGVPEKANI HGTYI KKA  
RSPaV-124.4K MNVL VKALS AFEFVGVS VL.KFPVVI HSPVGS GKSSLI RELI SEDENFI AFTAGVPDSPNL TGRYI KPY

Majority #.G....G#...\*LDEY\*...\*\*...LF\*DP\*Q.N.#....A\*F\*#....RFG..T#...L....G...#.  
PVM25K S-GQQPEGKFVVLDEYTL.TEVPPVFALFGDPI QSNTSAVQRADFVCSVSRRFGSATCGLLRELGNVR  
ASPV25K RQQRGRGNYSI LDEYLSG.EYSTGFNCLFSDPYQ.NHGDCLRAHFI GRCSHRFGRQTVQI LRD LGYNI A  
RSPaV-124.4K SPGCAVPGKVNI LDEYLSV.QDFSGFDVLFSDPYQ.NISIPKEAHFI KSKTCRFGVNTCKYLS SFGFKVS

Majority ..S....D.V.#....\*#\*#...\*G\*...\*#...\*#...H.E.\*...\*#\*#\*G.TF.#VT...#.....#.  
PVM25K ..SEKADLVQVSDI YTKD.PLGKVVFS EEEVGCLLRSHGVEALS LQEI TGQTFEVVTFVTS ENSPVI NRA  
ASPV25K ..SSKEDI VEKKNIFQLI EPEGVI ICLEKGVEDFLK WHSVEYKFP CQVRGATFDI VTFI HEKPLEELVGP  
RSPaV-124.4K ..SDGLDKVI VGSPTLDV.EGVLI CFCKEAVDLAVAHNSEFKLPCEVRGSTFN VVTLKSRDPTPEDRH

Majority ...#.\*.TRHR.\*#\*#...  
PVM25K AA.YQCMTRHRLC.TSVS  
ASPV25K DL.FVALTRHRSKL.VLVSN  
RSPaV-124.4K WF.YI AATHREKL.IIMQ

FIG. 5A



Consensus	MP*.*.....P.....K.....*.*G.....#V*..L...S.LP..GD**H..PHGG.Y#DGTK#*.Y**P..*
PVM 12K	MP*.....LTPPPDFTKVYLSAALGVSLALVVWLLIRSTLPVVGDRDHNLP HGGWYRDGTSVFYNSP..G
ASPV 12K	MPFAQ.....PPDYSKSVFPIAVGI AVAVVLFTLTRSTLPQVGDNI HNLPHGGNYQDGTKRISYCGPRDS
RSPaV-112.8K	MPFQQ.....PANWAKTITPLTVGLGIGLVLFHFLRKSNNLPYSGDNIHQFPHGGRYRDGTSITYCGPKQS

[illegible]

**8/16**

**FIG. 5B**

**VSRAVEEI DYHC**

**FIG. 5C**

Consensus \*..TLR#.C..YA\*. \*WN..L.\*..PPA\*W#. \*F.....#A\*FD\*F.\*V.....#\*P..G..R.PT.\*E  
(188) PVMCP DAETLRRVCRLYAPVTWNHMLTHNAPPAEWAAMGFQVEDRFAPDFCFDYVENTAAVQPLEGLIRRPTPRE  
(301) ASPVCP EGCTLRQYCAFYAKHVWNLMLQTQSPPANWVGKEFKFETRYAADFDFFGVESTASLEPADGLIRLPTQAE  
(142) RSPaV-1CP EVTTLRRFCMYAKI VVNI HLETGIP PANWAKKGFNENEKFAAFDFFLGVTDES ALEPKGGI KRAPTKAE

Majority .VA\*...\*. \*R.#...\*. \*E..GG..G.....\*  
PVMCP KVAHNTHKDI AL·RGANRNQVFSSLNAEVTGGMNGPELTRDYVKS NRK  
ASPVCP RVANATSKEI QMYRI RSMEGTQAVNFGEVTGGKI GP...·KPVLSI·RK  
RSPaV-1CP MVANI ASFEVQVLRQAMAEGRSSNLGEISGGTAGALINNPF SNVTHE

10/16

FIG. 5D

Consensus  
ASPV 3'UTR  
RSPaV-1 3'UTR

...G.T.A...AA.TC...C...CA.TTC...T.CA.TA.TT...C...TTT...AA.G.TG...A.CCT...  
TTAGTTAATTAAATTCCTCGCA.TTCAAT..TTCAGTACTTATGCTTTTCTAGTAAGTTGATCCCAACCTAAC  
..GGATGACGAAGTCAGCGACAATTCCGCAGTCCAATAATCCCGATT..CAAGCTGGGTTAAGCCTGTT

Consensus  
ASPV 3'UTR  
RSPaV-1 3'UTR

CG..GG...C..T...GT..T...TT.CATGCT...A.C.TATTT...TGT...  
CG..GGCGGGCTATGT...GTGTGTTCTTTTCATGCTTACGCTTATTTT...TGT...  
CGCTGGAATACCGTACTAATAGTATTCCTTTCCATGCTAAATCCTATTATAATATAAGTGTGGAAAGTAA

Consensus  
ASPV 3'UTR  
RSPaV-1 3'UTR

...TTT...TAG.TTT...TC  
...TTTAAC...TAGATT...TC  
AAGAAGATTGGTGTGTTTATAGTTTCATTC

11/16

**FIG. 6A**

Consensus .....  
PVM 3' UTR .....  
RSPaV-1 3' UTR GGATGACGAAGTCAGCGACAATTCCGAGTCACAATAATCCCGATTTCAGGCTGGGTTAAGCCTGTTTCGCT

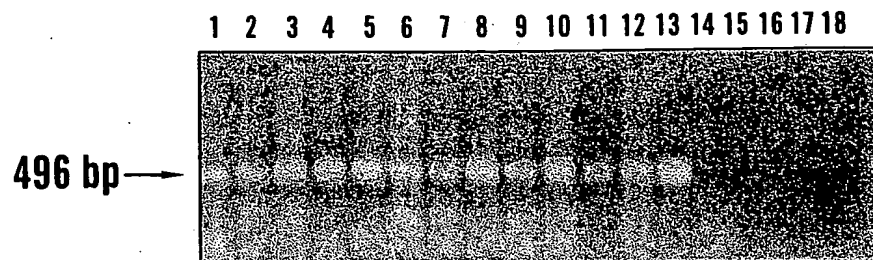
Consensus ..... CCAT.. TAAATCCTATTTAATATATAA. GTGTG.. A.... AAA. A  
PVM 3' UTR ..... CCAT.. TAAATCCTATTTAATATATAA. GTGTG.. A.... AAA. A  
RSPaV-1 3' UTR GGAATACCGTACTAATAGTATTCCTTCCATGCTAATCCTATTTAATATATAA. GTGTG.. A.... AAA. A

12/16

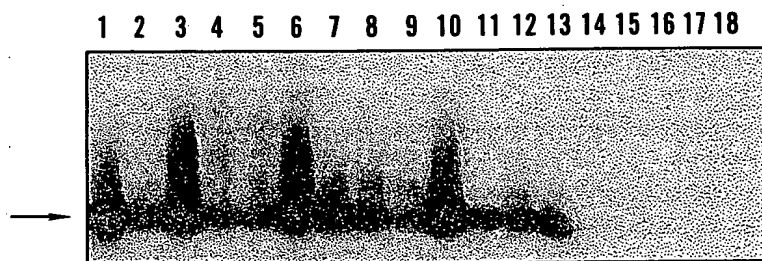
Consensus A. A. TTGGT. T. T... TAT... TTTT.....  
PVM 3' UTR AAAC TTGGT TTTT AACTAT... TTTTAGCCA  
RSPaV-1 3' UTR AGATT TGGTGTG TTTT TATAG TTTTCATTC

**FIG. 6B**

13/16



**FIG. 7A**



**FIG. 7B**

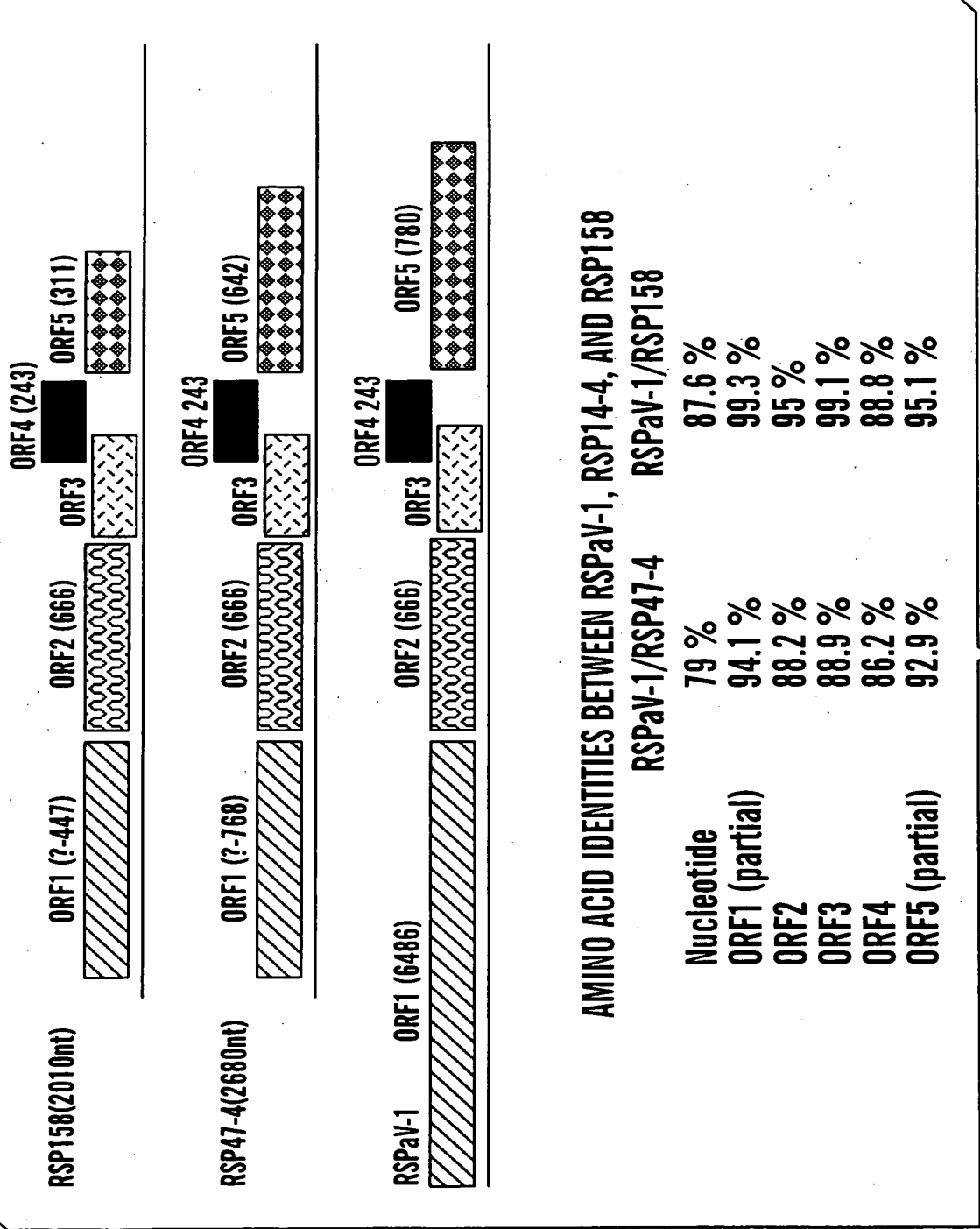


FIG. 8

15/16

FIG. 9

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.C.GG..T.AA.G.TGG.CA.TGTGT.ATTTT.GA.GAGGT.CAGTTGTTCC.CC.GGA.A.ATCGAT.T..G.T..CTT.T.A.ACG.AG.GA.GCTT

140/94-19T7+R1 GCAGGATTGAAGCTGCTCCTCTGTGTGATTTTGTGATGAGTCCAGTTGTTTCTCTGGATACATCGATCTATCTTGGCTTATTATACGTAGTGATGCTT
140/94-24T7+R1 TTTGGTTTGAAGCTGTCATTTGTGTGATTTTGTGATGAGTTCAGTTGTTTCTCTGGATACATCGATCTGTTTACTTGTATACGATGATGCTT
140/94-2T3+F1RC GCAGGTCTAAAGCTGGTCACTGTGTGATTTTGTGATGAGTCCAGTTGTTTCTCTGGATACATCGATCTATGTTTCTTATTATACGTAGTGATGCTT
140/94-42T3RC GCAGGTCTAAAGCTGGTCACTGTGTGATTTTGTGATGAGTCCAGTTGTTTCTCTGGATACATCGATCTATGTTTCTTATTATACGTAGTGATGCTT
140/94-64T7+R1RC GCAGGTTGAAGCTGGCTCACTGTGTGATTTTGTGATGAGTCCAGTTGTTTCTCTGGATACATCGATCTATGTTTCTTATTATACGTAGTGATGCTT
140/94-6T3+F GCAGGTTGAAGCTGGCTCACTGTGTGATTTTGTGATGAGTCCAGTTGTTTCTCTGGATACATCGATCTATGTTTCTTATTATACGTAGTGATGCTT
140/94-72T7+R1 TTTGGTTTGAAGCTGGTCACTGTGTGATTTTGTGATGAGTCCAGTTGTTTCTCTGGATACATCGATCTATGTTTCTTATTATACGTAGTGATGCTT
RSPv-1 GCAGGTTGAAGCTGGCTCACTGTGTGATTTTGTGATGAGTCCAGTTGTTTCTCTGGATACATCGATCTATGTTTCTTATTATACGTAGTGATGCTT

T.ATTT.ACT.GC.GGTGA.CCATG.C..AGCATATGA.TC.CA.AA.GATCG.GC.ATTTTGGG.GCTGAGCAGAGTGACATACT.A.A.T.CTTGA

140/94-19T7+R1 TCATTTCACTTGGCTGTGATCCATGTCATGACAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA
140/94-24T7+R1 TCATTTCACTTGGCTGTGATCCATGTCAGAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA
140/94-2T3+F1RC TCATTTCACTTGGCTGTGATCCATGTCAGAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA
140/94-42T3RC TCATTTCACTTGGCTGTGATCCATGTCAGAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA
140/94-64T7+R1RC TCATTTCACTTGGCTGTGATCCATGTCAGAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA
140/94-6T3+F TCATTTCACTTGGCTGTGATCCATGTCAGAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA
140/94-72T7+R1 TTTATTTCACTTGGCTGTGATCCATGTCAGAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA
RSPv-1 TCATTTCACTTGGCTGTGATCCATGTCAGAGCACATATGATTCGAAAGGATCGGCCAATTTTGGCGCTGAGCAGAGTGACATACTTAGAATGCTTGA

.GG.AA.AC.TATAGGTA.AACAT.GAAAGCAG..G.TTTGTGAA.CCAATGTT.GAAT...GACT.CCATGTCA.TTCAAAA.GGG...C.ATGACTGC

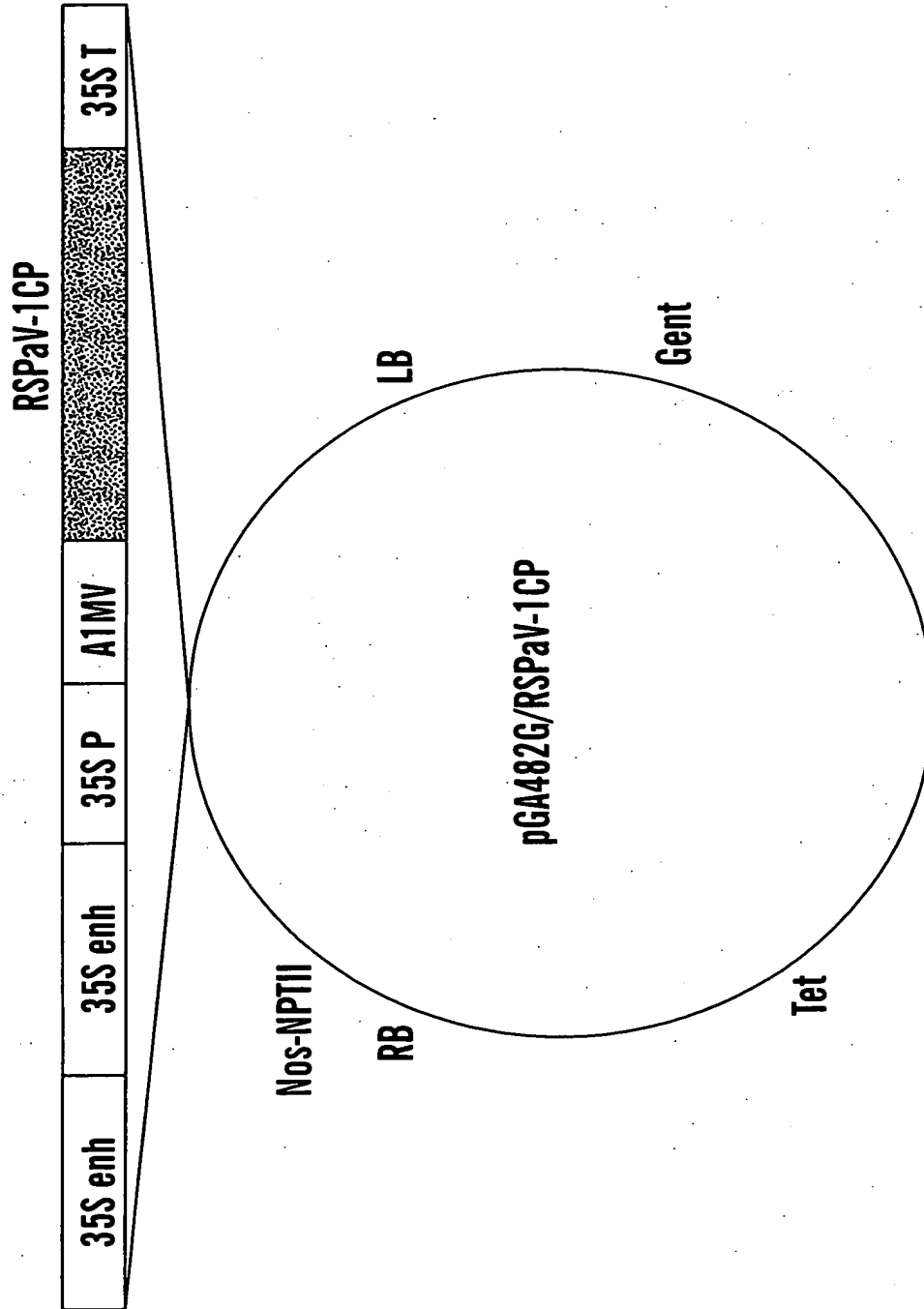
GGGCAAAACGTATAGGTATAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCAGACTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
AGGAAAGAGTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTAGACTACCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
AGGCAAGAGCTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
AGGCAAGAGCTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
GGGCAAGAGCTATAGGTATAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
GGGCAAGAGCTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
GGGCAAGAGCTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
GGGCAAGAGCTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
GGGCAAGAGCTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC
GGGCAAGAGCTATAGGTACAACATAGAAAGCAGGAGTTTGTGAACCAATGTTTGAATCTGAGCTGCGCATGTCACTTCAAAAA-GGGTTTCAATGACTGC

.GC.TT.GCTGATTATGC.AT.TT.....

140/94-19T7+R1 CGCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTCCAGTTTTCAGGAG
140/94-24T7+R1 AGCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTCCAGTTTTCAGGAG
140/94-2T3+F1RC TTTCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTTCAGTTTTCAGGAG
140/94-42T3RC TTTCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTTCAGTTTTCAGGAG
140/94-64T7+R1RC CGCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTTCAGTTTTCAGGAG
140/94-6T3+F CGCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTTCAGTTTTCAGGAG
140/94-72T7+R1 TTTCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTTCAGTTTTCAGGAG
RSPv-1 CGCTTTGCTGATTATGCAATCTTCCATAATATGCAATGACTTCTCTGGCAGGTCAAAGGTCCTTTGGATGCCGTTTGGTTTCAGTTTTCAGGAG
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16/16



**FIG. 10**